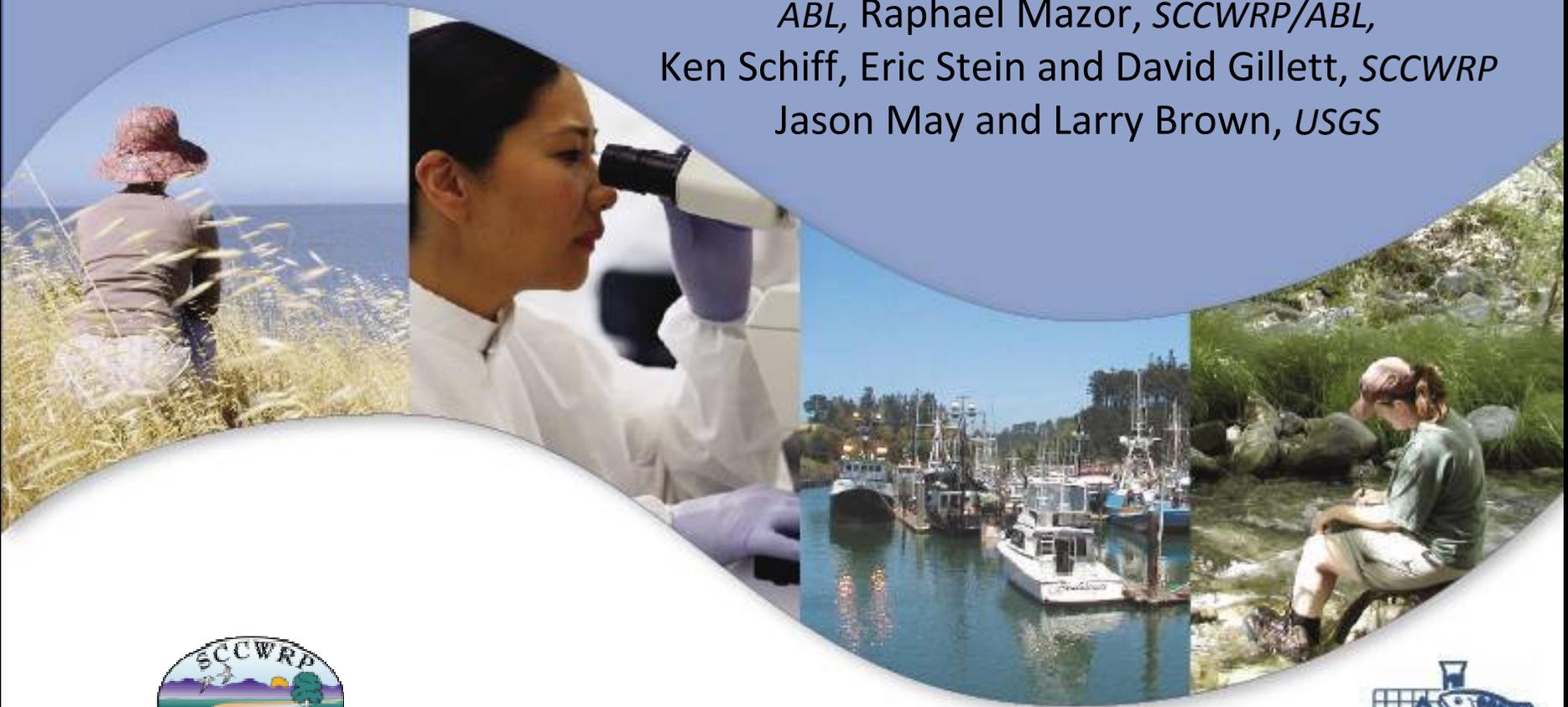


# Bio-objectives: Initial Technical Steps

Peter Ode, *SWAMP/DFG-ABL*, Andrew Rehn, *DFG-ABL*, Raphael Mazor, *SCCWRP/ABL*, Ken Schiff, Eric Stein and David Gillett, *SCCWRP* Jason May and Larry Brown, *USGS*



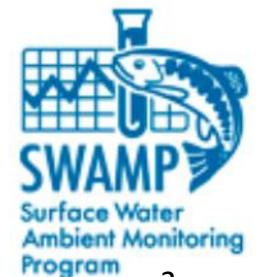
# Steps I and II: Define reference criteria and develop scoring tools

## Reference

- Background and Objectives
- Final Criteria and Performance Evaluation

## Scoring Tools

- Background
  - MMIs and Predictive Models
- Predictive Model Development Update
- Next steps



# Reference Philosophy and Objectives

Reference condition is the foundation of bio-objectives  
= **objective** basis for **uniform biological standards**

- Use natural condition (or something close to it) as the desired state whenever possible
- Expectations must accommodate CA's diverse ecological and landuse settings, but retain **consistent** meaning throughout the state
- **Objective** = effective/well-supported scoring tools

# Balancing Type I and Type II error

(risks of keeping stressed sites in the reference pool vs. rejecting low stress sites, respectively)

In a perfect world with a large number of undisturbed streams of all types, we could focus exclusively on Type I error

However, very restrictive criteria result in under-representation of important natural gradients. Thus, Type II error (excessive rejection of sites) reduces the performance and applicability of our scoring tools

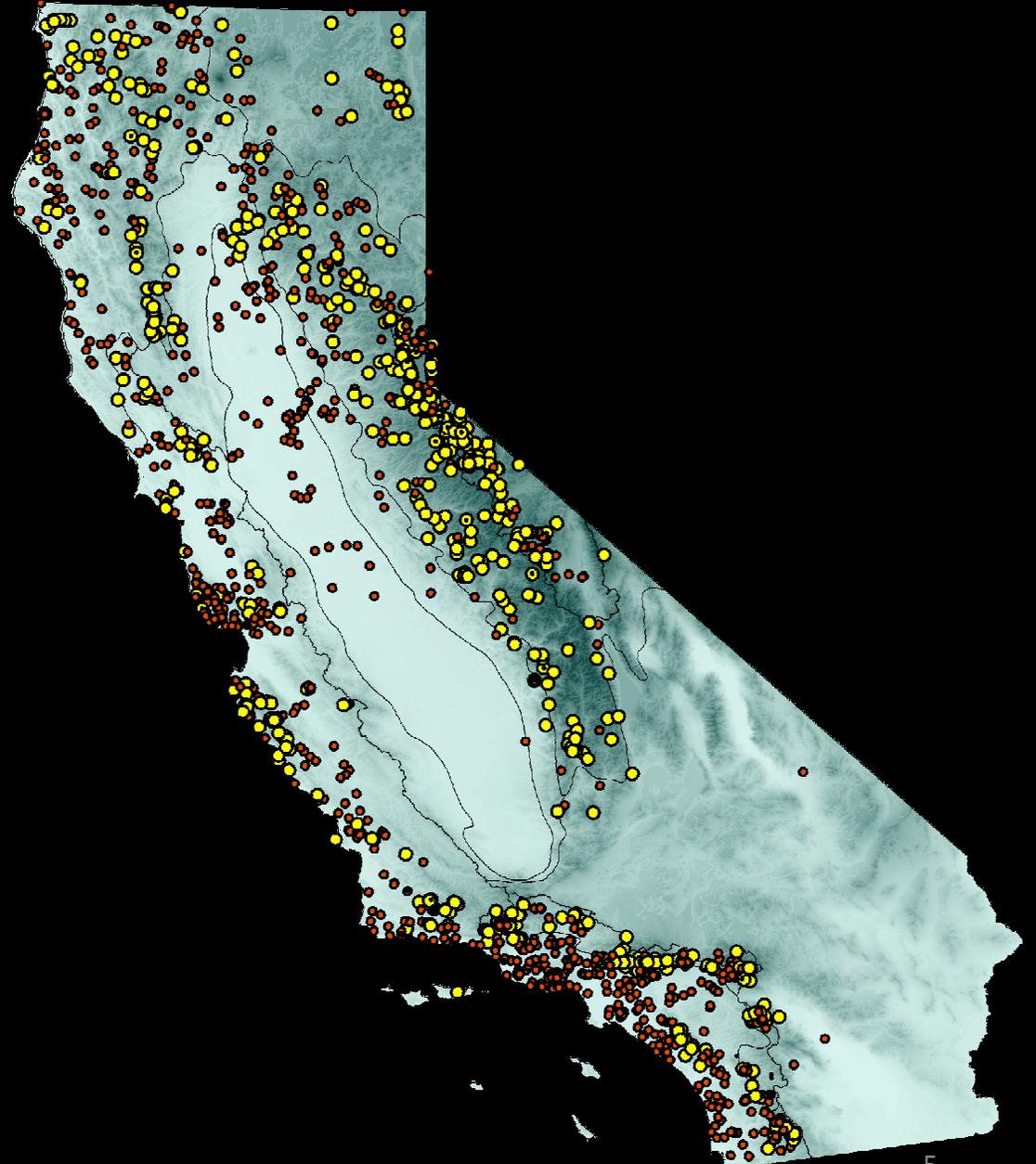
## ***Performance Measures:***

*i) did we adequately represent important gradients?*

*ii) did we retain biological integrity of reference sites?*

# Reference Sites

REGION	n
North Coast	79
Central Valley	1
Coastal Chaparral	87
Interior Chaparral	30
South Coast Mountains	96
South Coast Xeric	22
Western Sierra	131
Central Lahontan	142
Deserts + Modoc	27
<b>TOTAL</b>	<b>615</b>



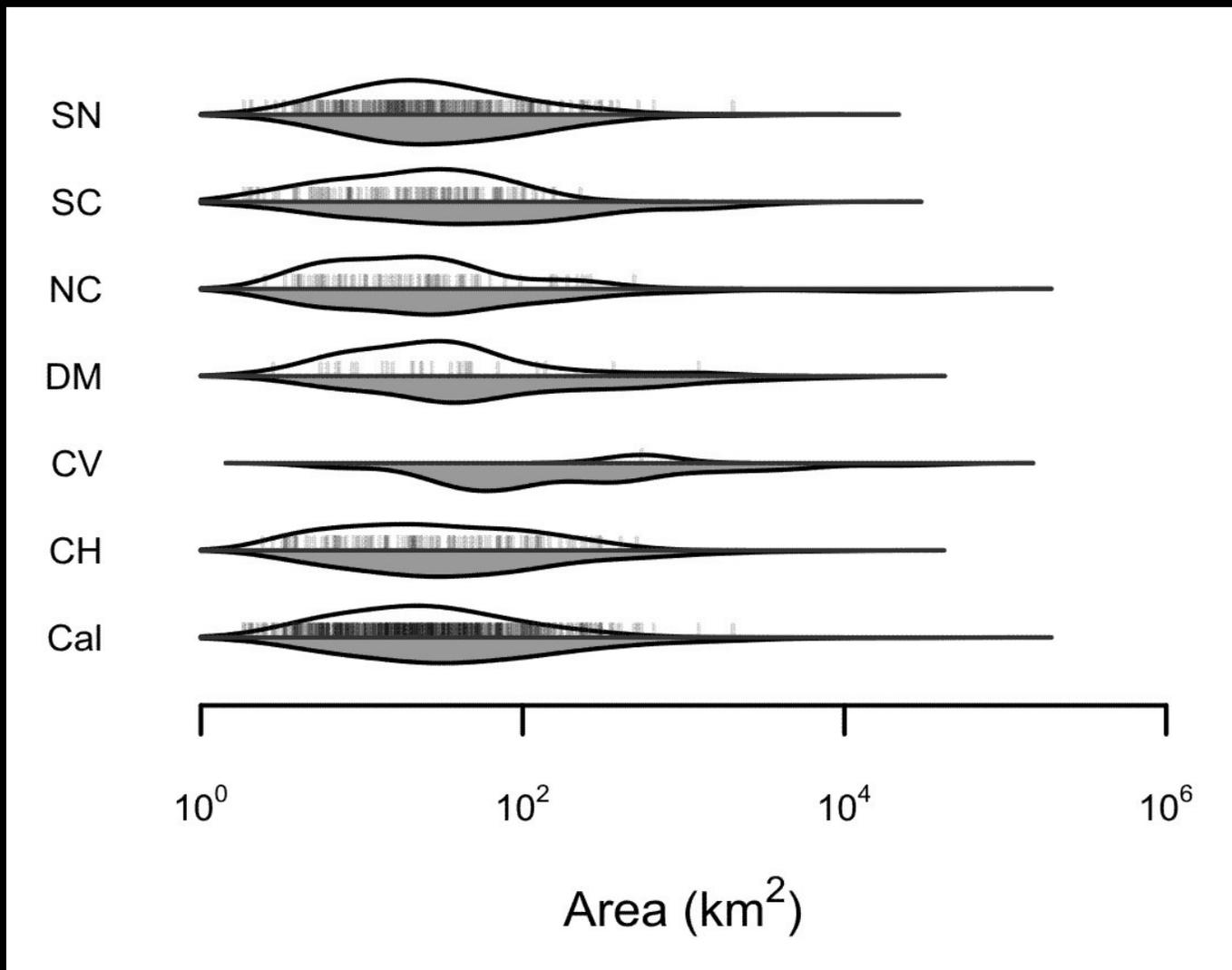
# Reference Site Count and % by PSA Region

(% estimated by PSA probability distributions)

REGION	n	% of region
North Coast	79	28
Central Valley	1	2
Coastal Chaparral	87	18
Interior Chaparral	30	33
South Coast Mountains	96	68
South Coast Xeric	22	2
Western Sierra	131	50
Central Lahontan	142	74
Deserts + Modoc	27	56
<b>TOTAL</b>	<b>615</b>	-

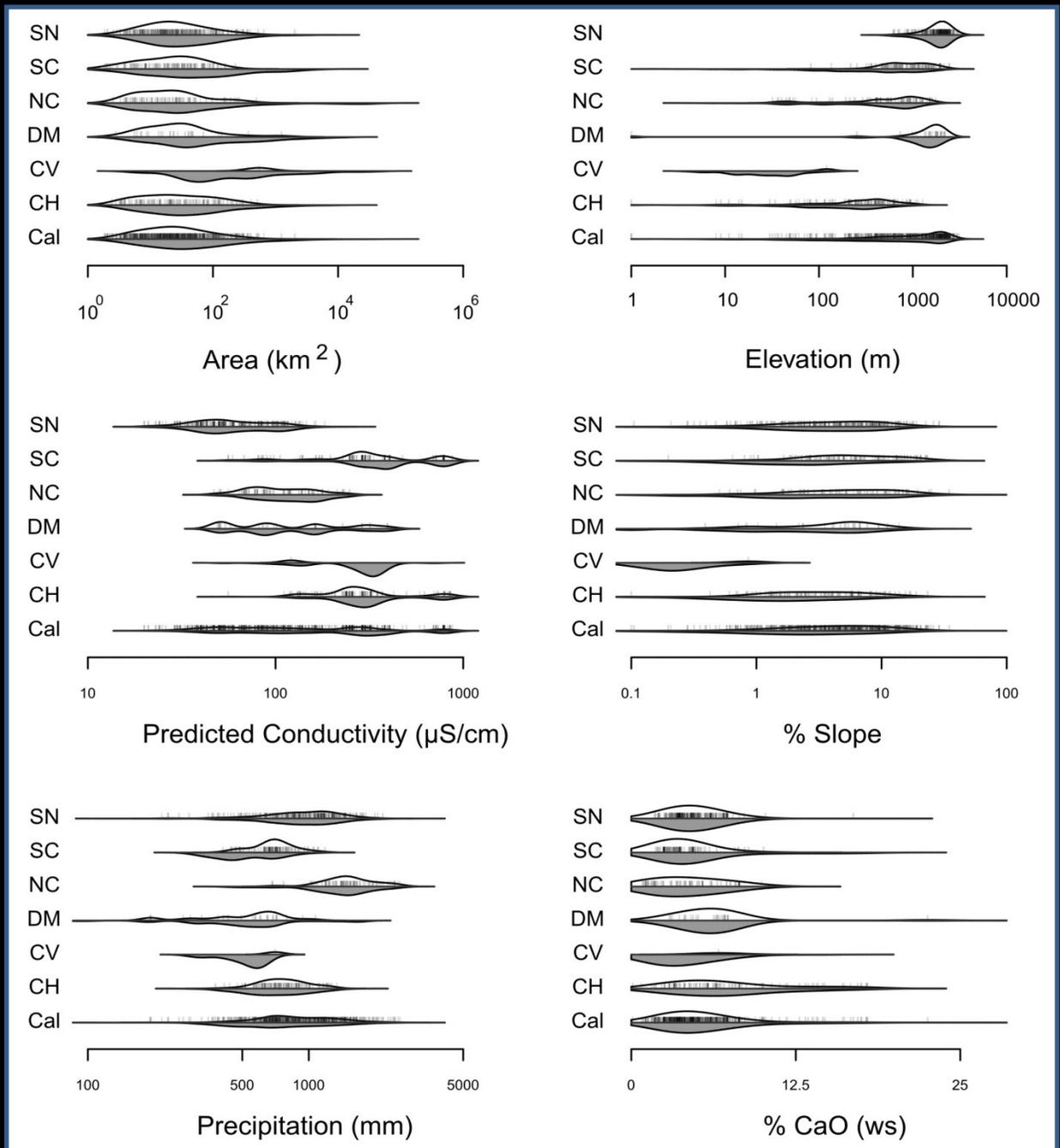
# Environmental Representativeness:

“Beanplots” used to compare match between reference and overall distributions



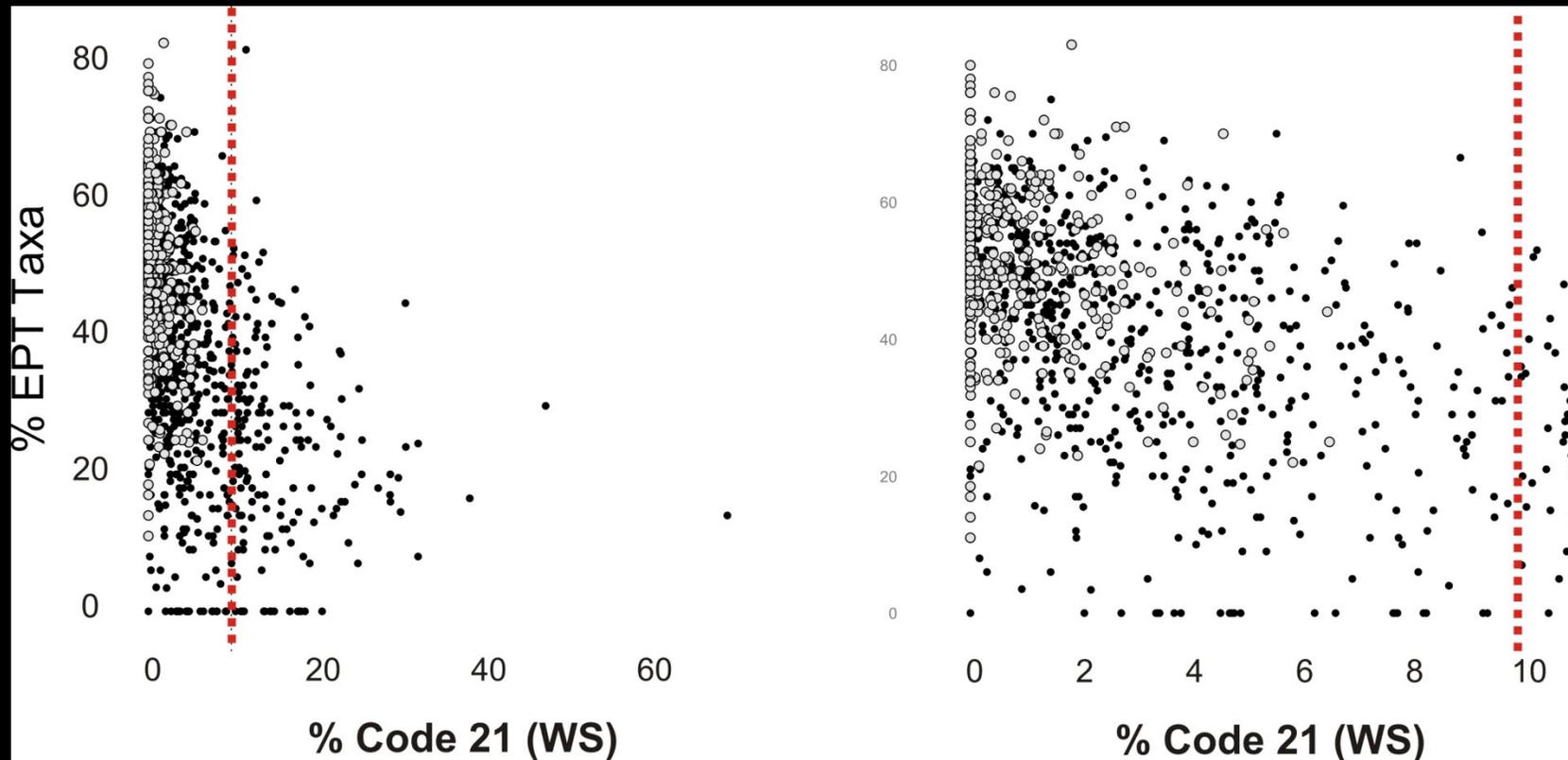
# Gradient Representation

- Overall excellent representation in most regions
- Central Valley and South Coast (xeric only) very under-represented
- Very low gradient, large watershed, low elevation settings slightly under-represented in Chaparral/ S. Coast



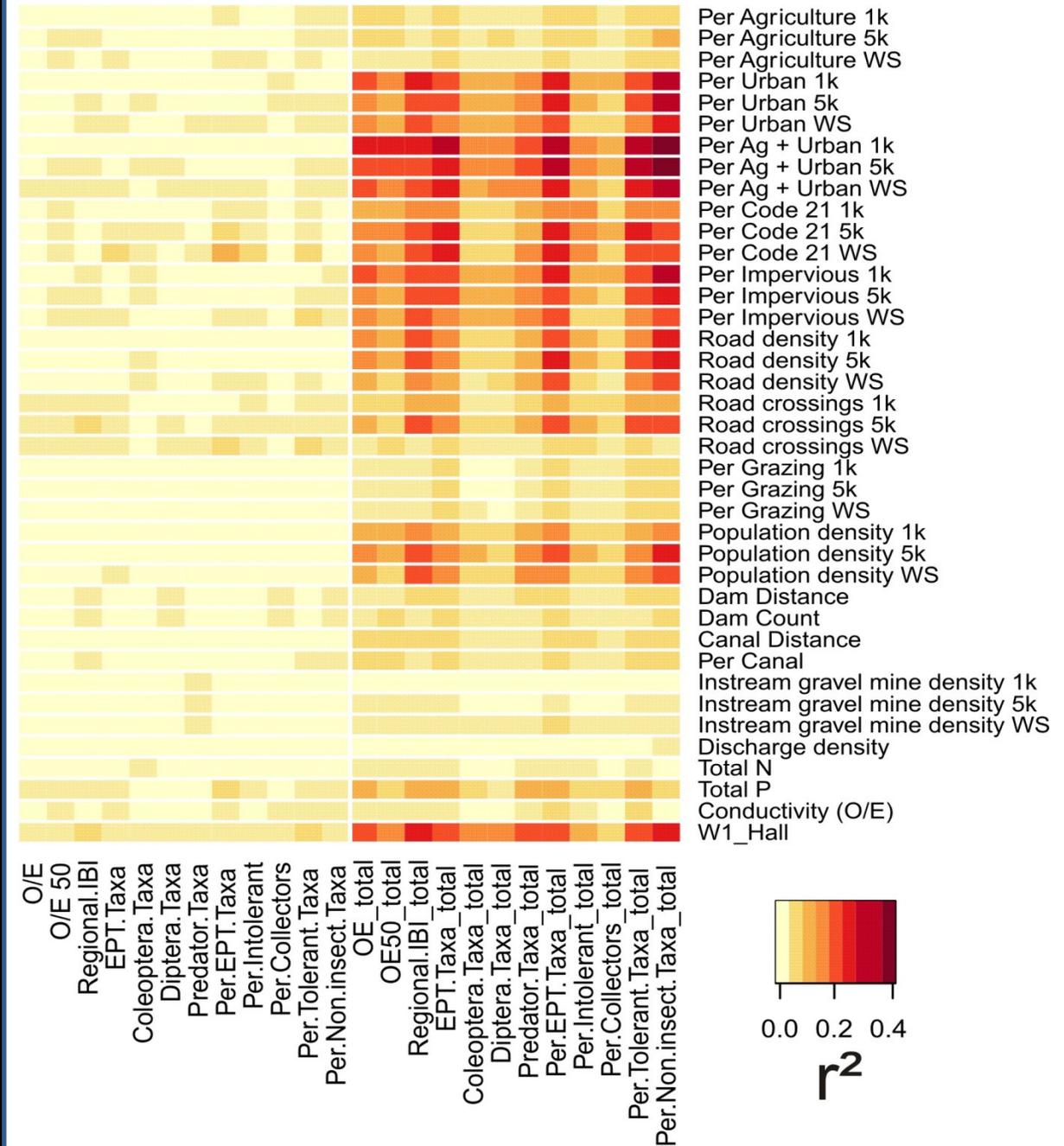
# Biological Integrity

Scatterplots of reference and all sites



# Biological Integrity

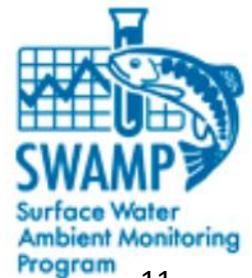
- “Heatmap” of biological variation related to various stressors in both the reference population (left) and across all sites (right)
- Anthropogenic sources of variation were generally low in the reference pool



# Questions for Science Panel

(similar to April questions)

- Did we achieve our objectives?
- Is the work adequately documented?
- Can we expect our reference pool to support robust regulatory standards?





# Scoring Tools:

## Two tools for measuring biotic condition

PRIMARY CHALLENGE: How to translate a list of organisms occurring at a site into a measure of biotic condition?

Two common approaches: **multimetric indices** (e.g., IBIs, widely used in US) and **predictive models** (e.g., RIVPACS, used in UK and Australia) ...

**HYBRID APPROACHES** are also possible

# Multi-metric (MMI) and predictive (O/E) models convert taxa lists to biological condition scores

## MMI (IBIs)

- *Convert taxa list to metrics (e.g., # mayfly taxa, % scraper taxa )*
- Can incorporate ecological function into assessments
- Easy to calculate
- Can evaluate component metrics independently

## Observed/Expected (O/E)

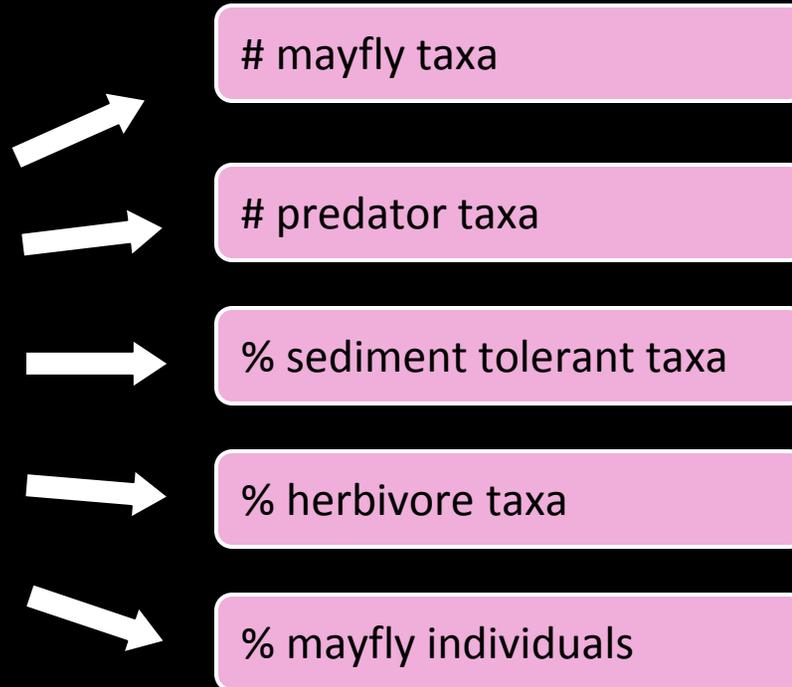
- *Directly compare observed taxa to those expected to occur in reference state*
- Are well suited to site-specific conditions
- Facilitate comparable assessments across broad regions

# Multimetric Indices: Index of Biotic Integrity (IBI)

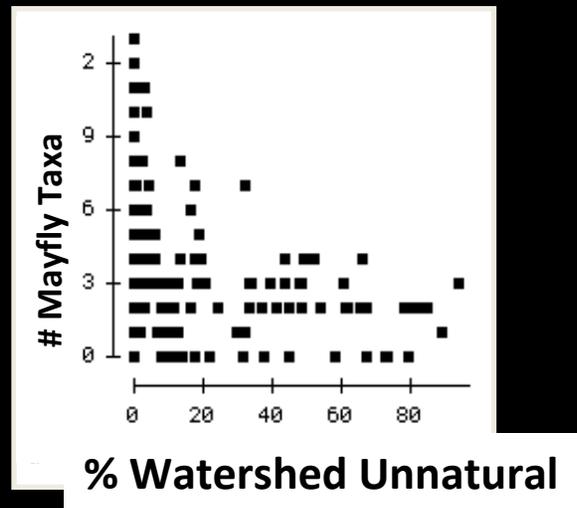
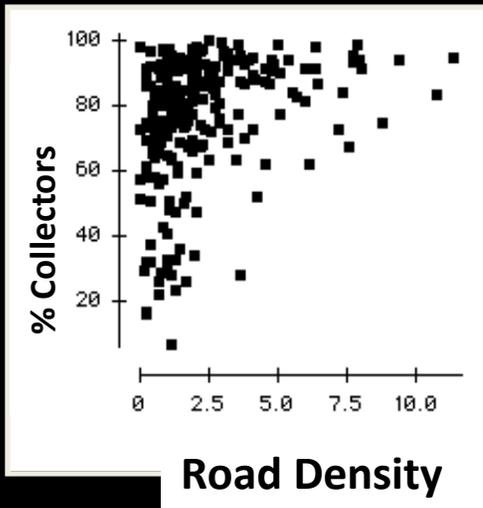
*Originally developed by James Karr (early 1980s) for Ohio fish assemblages;  
used widely in US for fish and BMIs*

Step 1. Organism list is converted into metrics

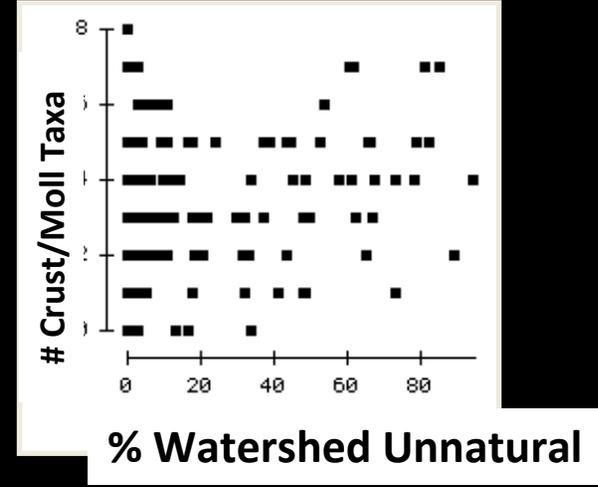
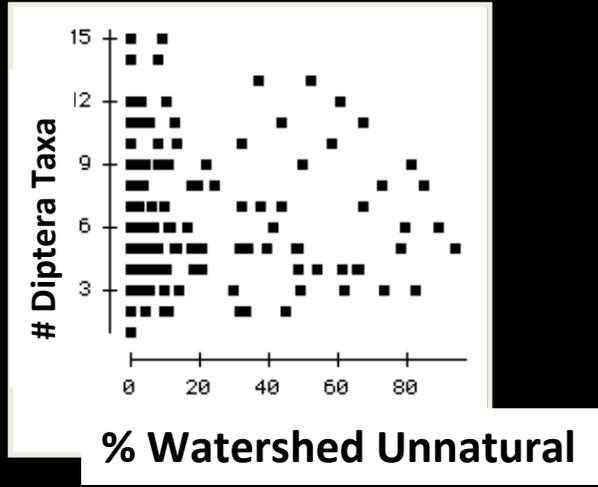
<u>Taxon</u>	<u>Count</u>
Mayfly species 1	43
Mayfly species 2	12
Mayfly species 3	2
Beetle species 1	1
Beetle species 2	1
Midge genus 1	65
Midge species 1	3
Midge species 2	10
Midge genus 2	3
Dragonfly species 1	2
Stonefly species 1	1
Stonefly species 2	14
Worm species 1	9
Worm species 2	2



# Step 2. Metrics are evaluated for performance (e.g., responsiveness to key stressor gradients)

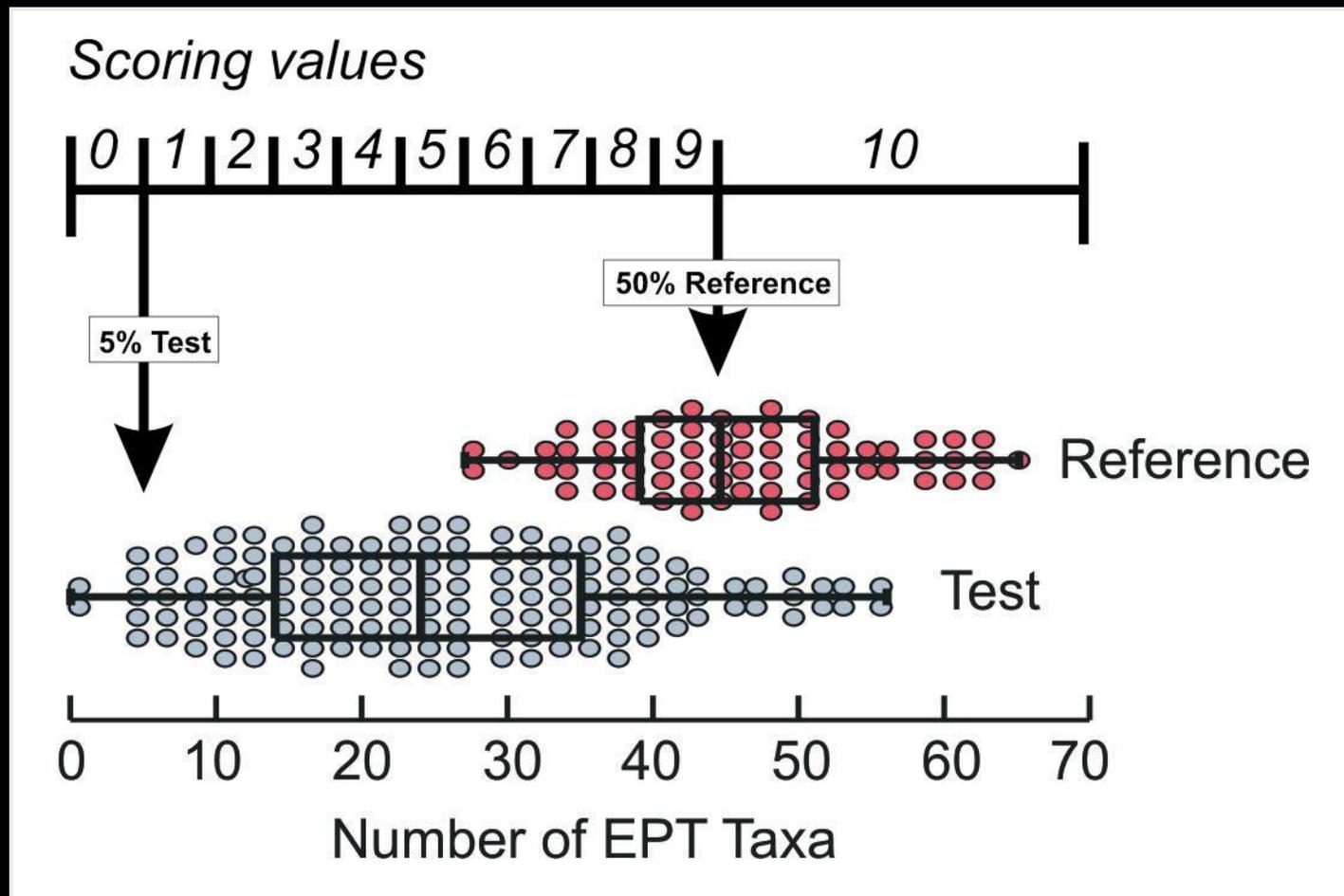


Responsive Metrics

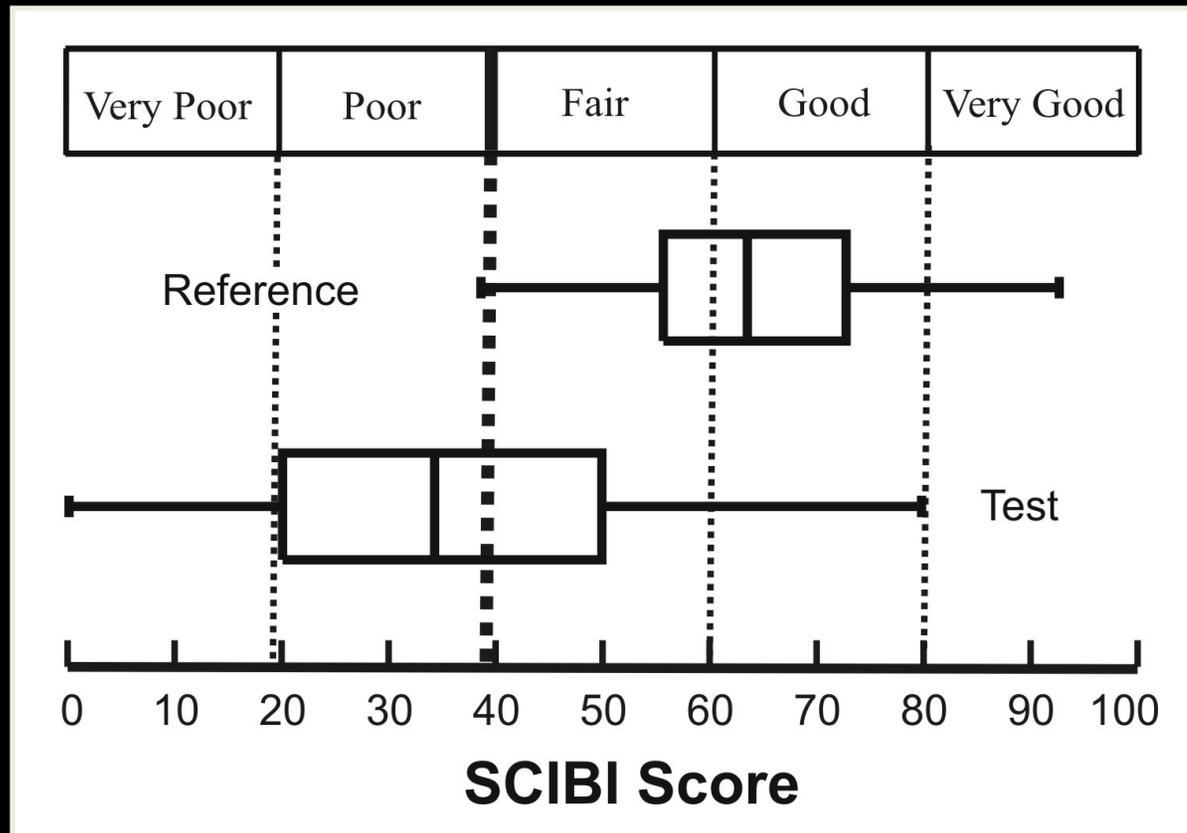


Not-so-responsive Metrics

Step 3. Metrics are scored based on distribution of metric values in reference sites vs. non-reference sites



## Step 4. Metric scores are assembled into index



Step 5. Index can be divided into “condition classes” for management interpretation  
(e.g., impaired/ not-impaired or good, fair, poor)

# Predictive Models: (Observed/ Expected Models)

*Developed in UK (Wright and others 1970s-1980s, RlvPACS),  
adapted in Australia (AusRivAS) and US (Chuck Hawkins, Utah  
State... source of most of these slides)*

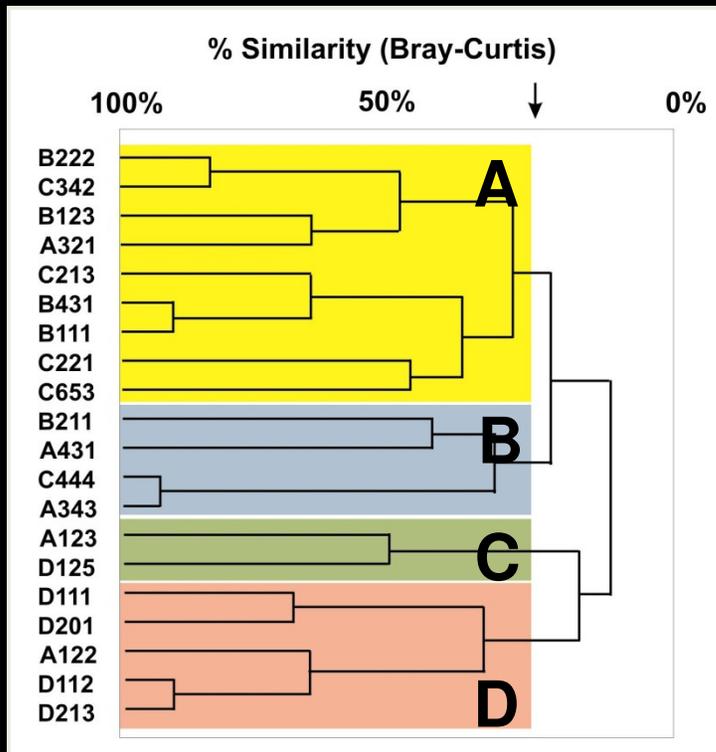
**Species-based approach:** Compare number of **observed** (“O”) taxa to number of **expected** (“E”) taxa

“Expected” taxa derived from predictive modeling techniques

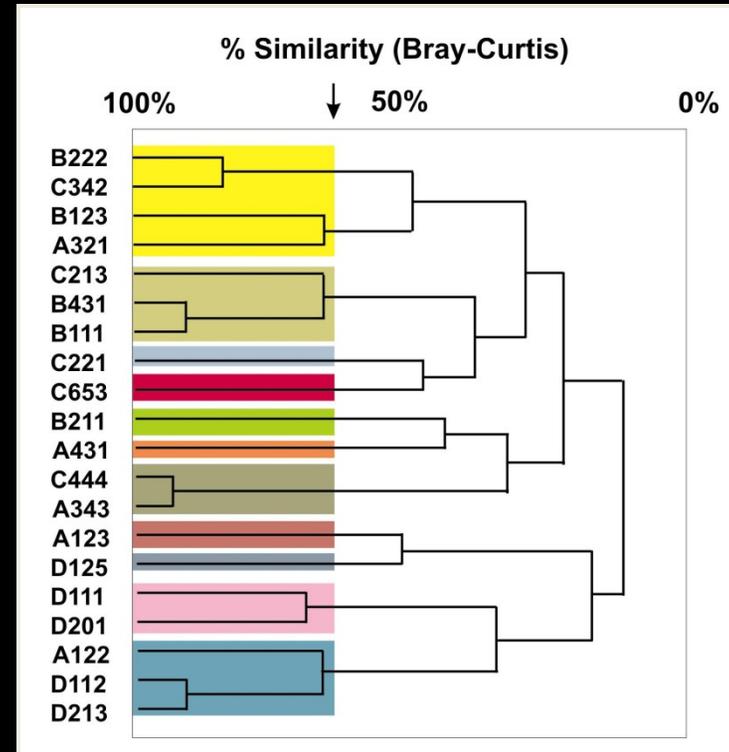
# Estimating “E”

Step 1. Classify reference sites based on biological similarity

Clustering techniques used to identify groups of reference sites with similar species composition



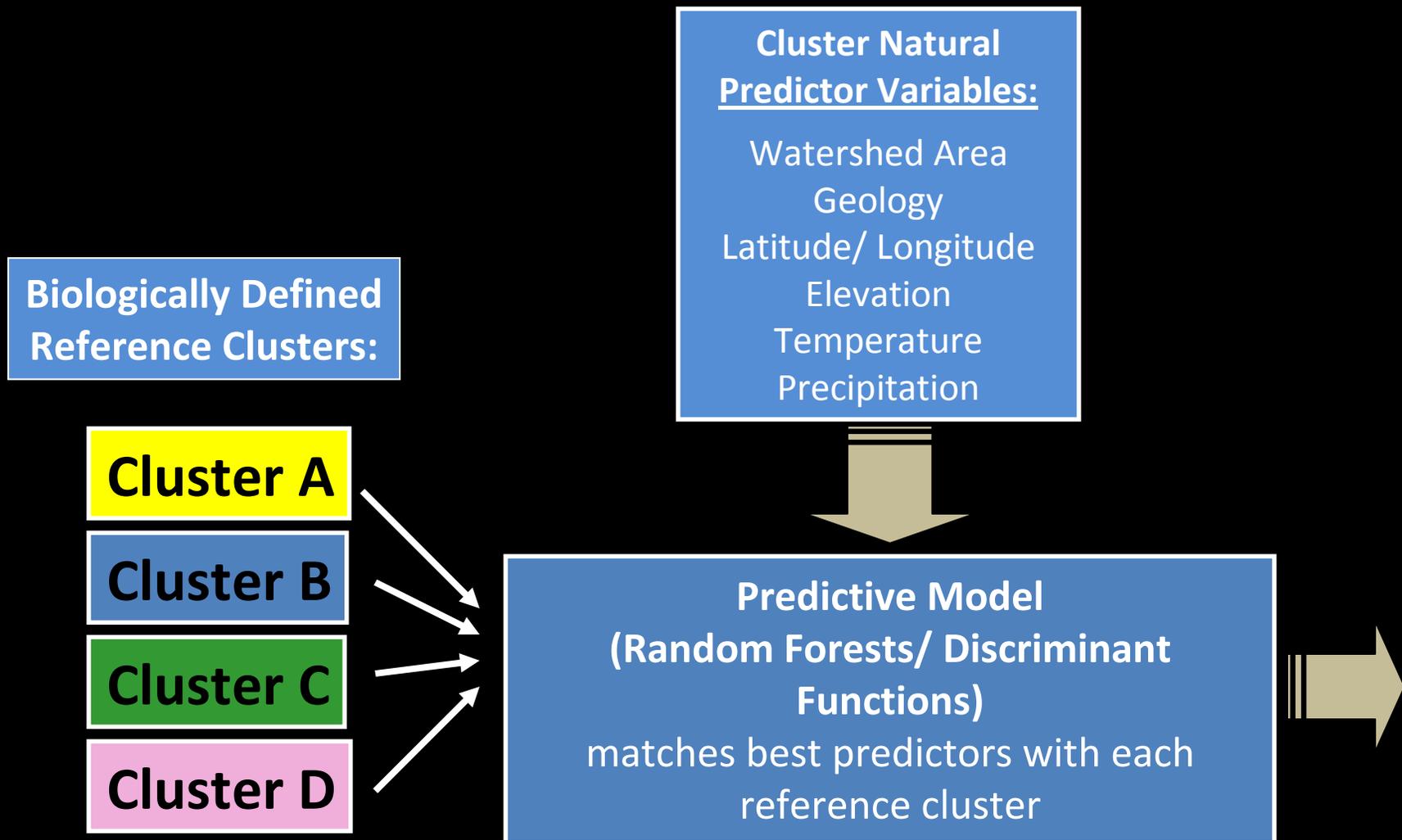
4 classes



11 classes

# Estimating "E"

Step 2. Develop model that will predict class membership for new sites



# Estimating “E”

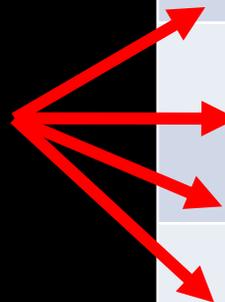
## Step 3. Estimate capture probabilities

Use discriminant model output + frequencies of occurrence within each class to estimate **probabilities of capture (PC)** for each taxon at a given site

Predictor Variables



Predictive Model  
(matches predictors with each reference class)



Cluster	Site's probability of cluster membership	Frequency of species X ( <i>Farula sp.</i> ) in cluster	Expected contribution to PC
A	0.5	0.6	0.30
B	0.4	0.2	0.08
C	0.1	0.0	0.00
D	0.0	0.0	0.00
Probability of <i>Farula sp.</i> being in sample if site is in reference condition			0.38

# Estimating “E”

Step 4. Sum of taxon occurrence probabilities is an estimate of the number of native taxa (E) that should be observed (O)

Taxon	pc	O
<i>Atherix</i>	0.70	*
<i>Baetis</i>	0.92	*
<i>Caenis</i>	0.86	
<i>Drunella</i>	0.63	
<i>Epeorus</i>	0.51	*
<b><i>Farula</i></b>	<b>0.38</b>	
<i>Gyrinus</i>	0.07	
<i>Hyaella</i>	0.00	*
E	4.07	3

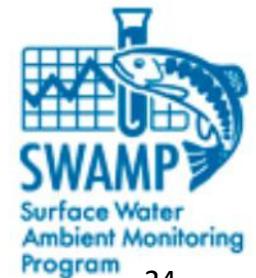
$$O/E = 3 / 4.07$$

$$O/E = 0.74$$

O/E (scaled 0.0 to 1.0):  
represents proportion of  
native assemblage present  
at test site

# Scoring Tool Goals

- **For Spring Science Panel Meeting (April 2012):**
  - fully explore both MMI and O/E approaches
  - test a variety of permutations and coordinate with regulatory panel
  - establish draft version of models for regulatory use
  
- **For today:**
  - Provide context for discussions on regulatory framework and pilot study
  - Show our initial steps to give a sense of what's ahead

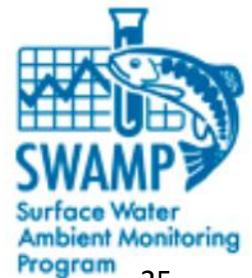


# O/E Major Steps

(variations at each step can influence model performance)

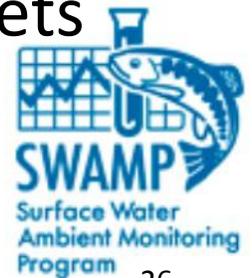
- *Data preparation*
- *Clustering*
- *Modeling*
- *Performance evaluation*

*Special thanks to Chuck Hawkins and John Van Sickle for advice and a great library of R scripts)*



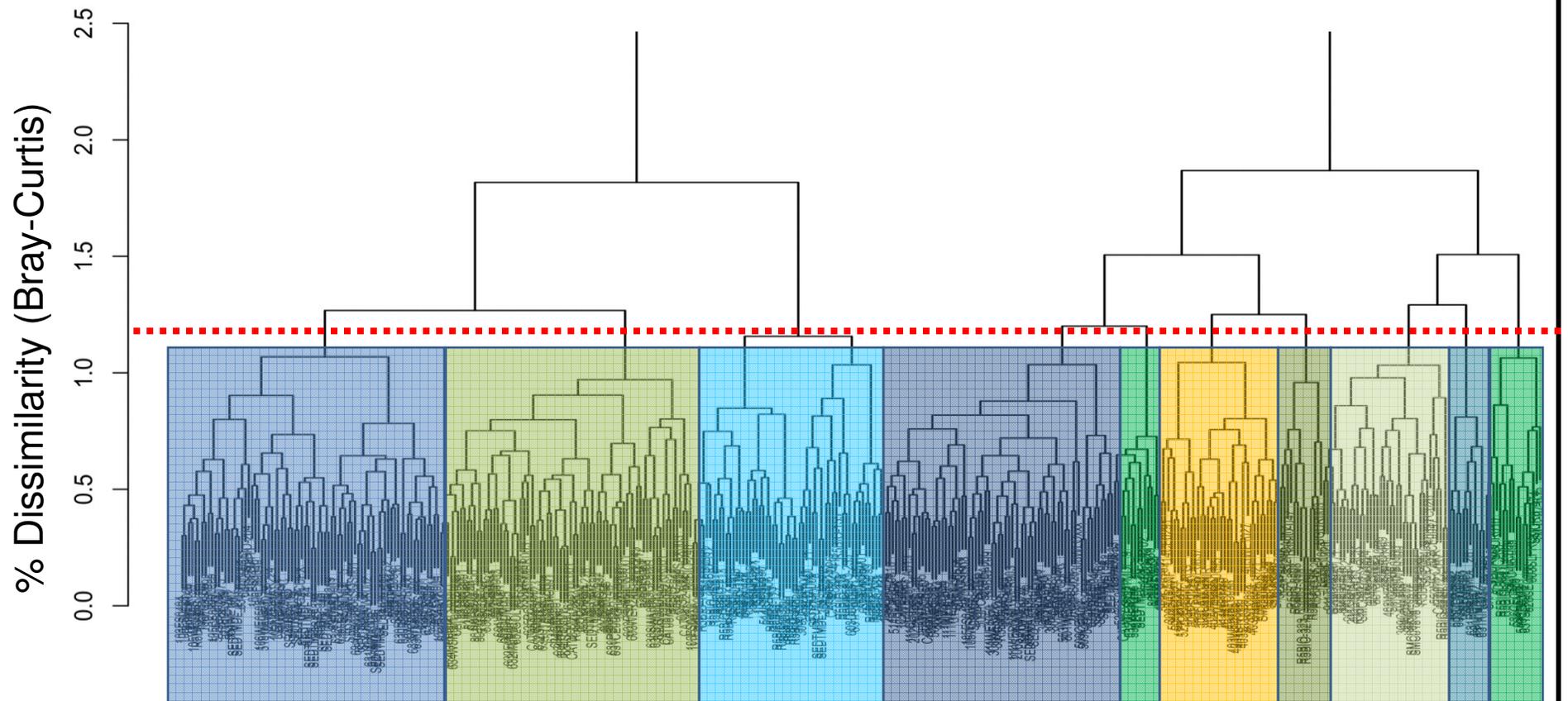
# Step 1: Data Preparation & Initial Decisions

- 615 reference sites identified in reference project
- Taxonomic Effort standardized at SAFIT I (a): mostly genus level IDs, with Diptera: Chironomidae to subfamily
  - After removing ambiguous taxa, **515 sites available for modeling**
- Prepare 34 **natural** predictor variables (pulled from reference screening dataset)
- Split dataset into **development** and **validation** sets (80:20, 410 sites in development set)



# Step 2: Cluster biological similarity

*(Bray-Curtis dissimilarity, flexible- $\beta = -0.25$ , rare taxa removed if  $< 2.5\%$  of sites)*



# 10 biological clusters

- Several large, geographically coherent clusters (e.g., blue, pink, black, green)
- Several pockets of high variability



# Step 3: Model predictor - environment associations

(**Random Forest** and Discriminant Functions)

Started with Random Forest models (plus enough DFA to make sure we can run the scripts!)

**Example for today:** explore role of cluster number and separate climate models

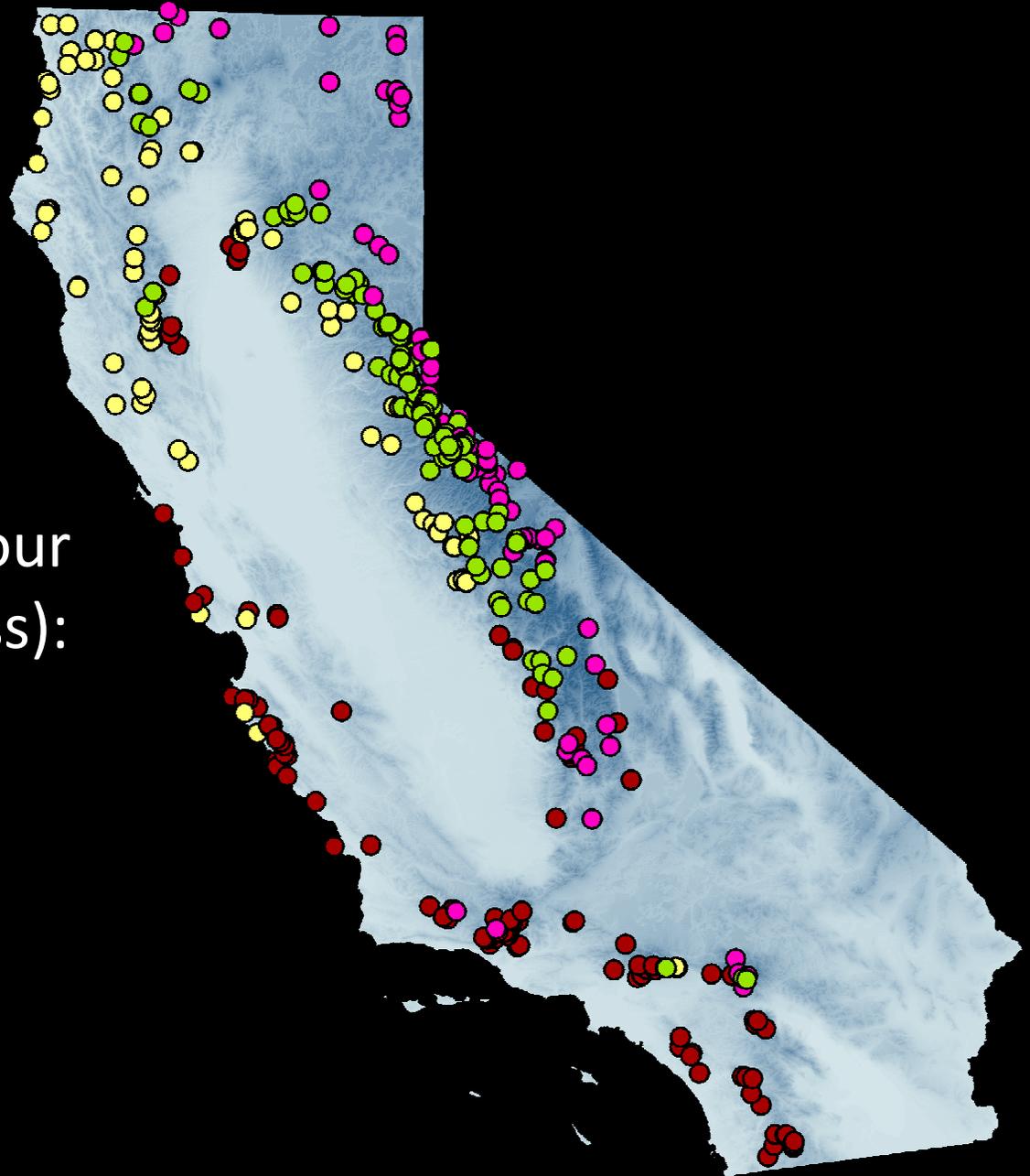
1. Statewide model
2. Four separate models based on PPT-Temp similarity



# 4 climate models

Median temp and PPT values used to create four classes (~100 sites/ class):

- HOT- WET
- HOT-DRY
- COLD-WET
- COLD-DRY



# Similarity between biological and climate clusters



4 climate clusters

10 biological clusters

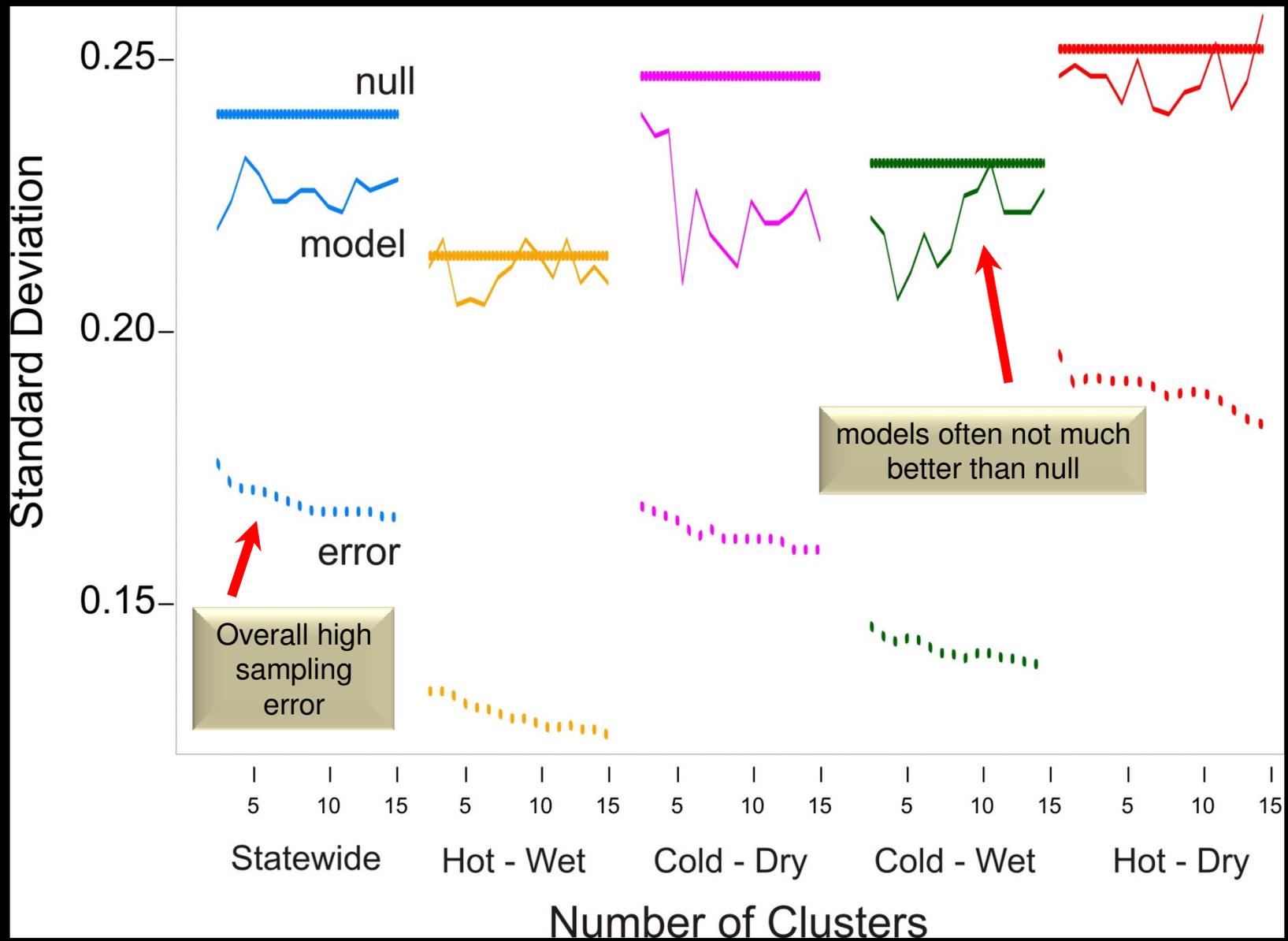
# Step 4: Evaluating Model Performance

## model precision, accuracy, bias

*(focus on precision for this example = standard deviation of O/E scores)*

- There is an intrinsic lower bound to SD that can be achieved by any model (commonly around 0.14, but can be as low as 0.11) = **replicate sampling SD**
- Upper bound is estimated by null model SD (no clusters, all sites compared equally to all other sites)



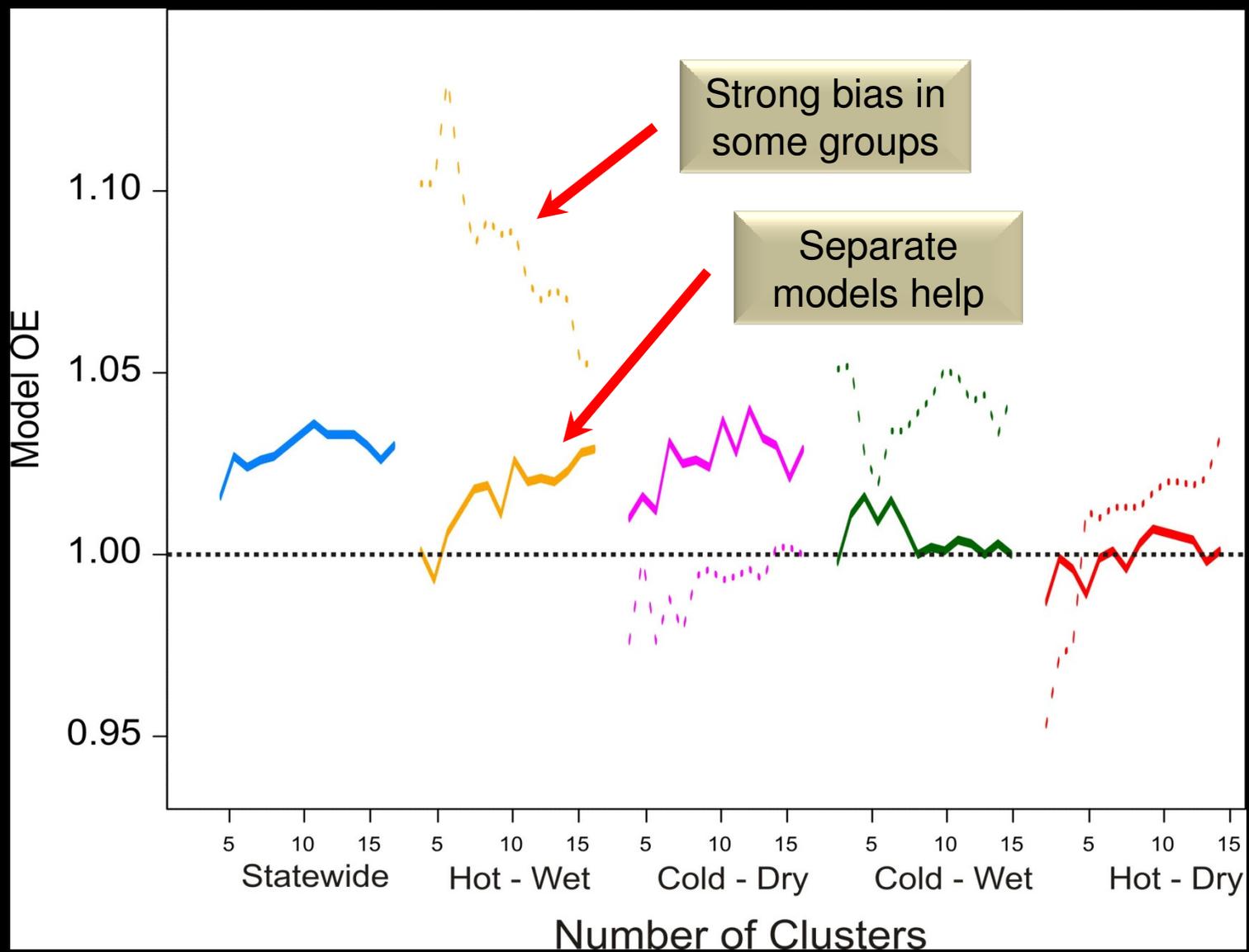




Each climate group modeled separately



Sub-group summaries using statewide model

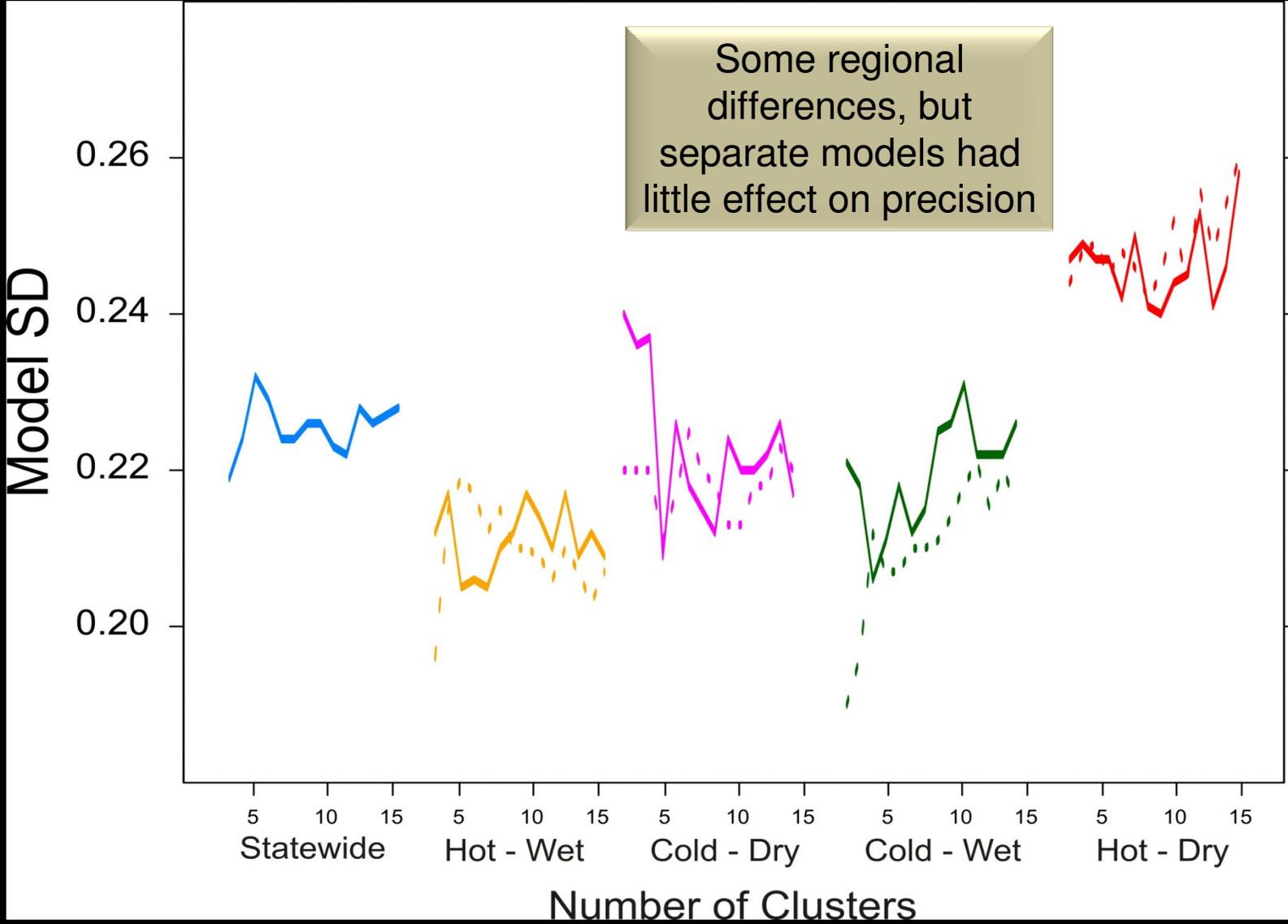




Each climate group modeled separately

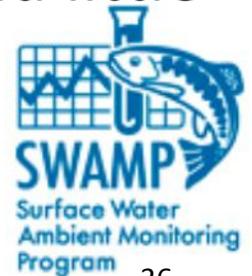


Sub-group summaries using statewide model



# Summary of initial results

- Overall high SD (low precision) for null, cluster models and sampling error.... we suspect that high biological variability is a consequence of our emphasis on “representativeness”
- Cluster number had little to do with performance
- Separate climate models improved bias, but had little effect on precision



# What's Next for O/E?

➤ Techniques are working and classification approaches have potential, but we have work ahead of us

➤ We intend to explore:

1. Predictors
2. Inter-annual climate variability
3. Classification techniques
4. Inclusion probabilities
5. Taxonomic effort levels
6. DFA Models

# What's Next for Scoring Tools?

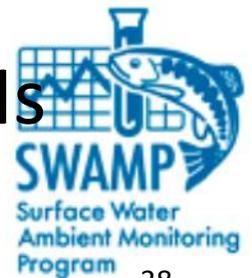
## ➤ **O/E:**

- Narrow down effective model parameters
- Evaluate more performance criteria (precision/sensitivity, accuracy, bias, responsiveness, etc.) both statewide and regionally

## ➤ **MMIs:**

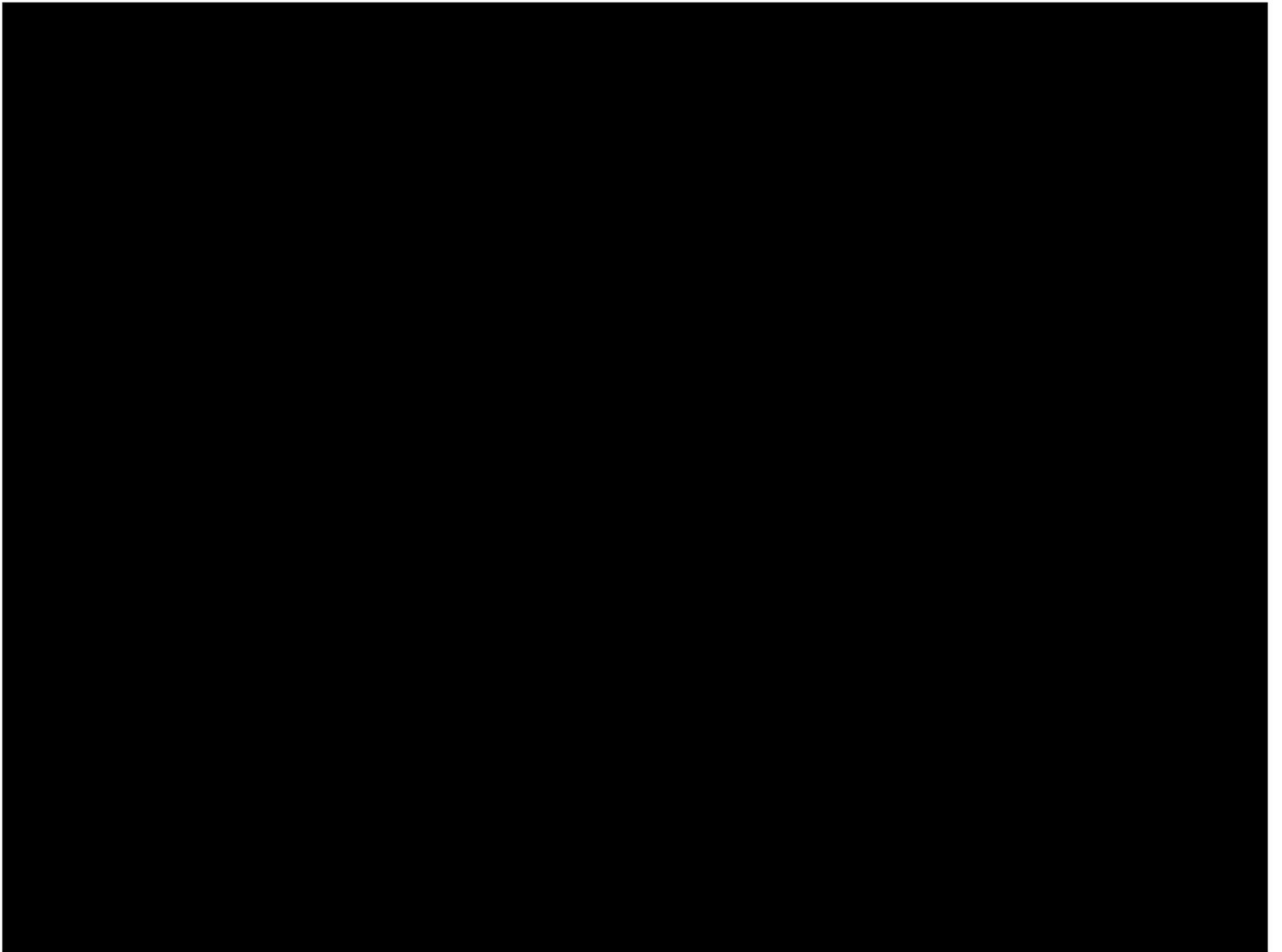
- Develop statewide and regional MMIs
- Compare performance to existing MMIs

## ➤ Explore potential MMI/OE hybrids



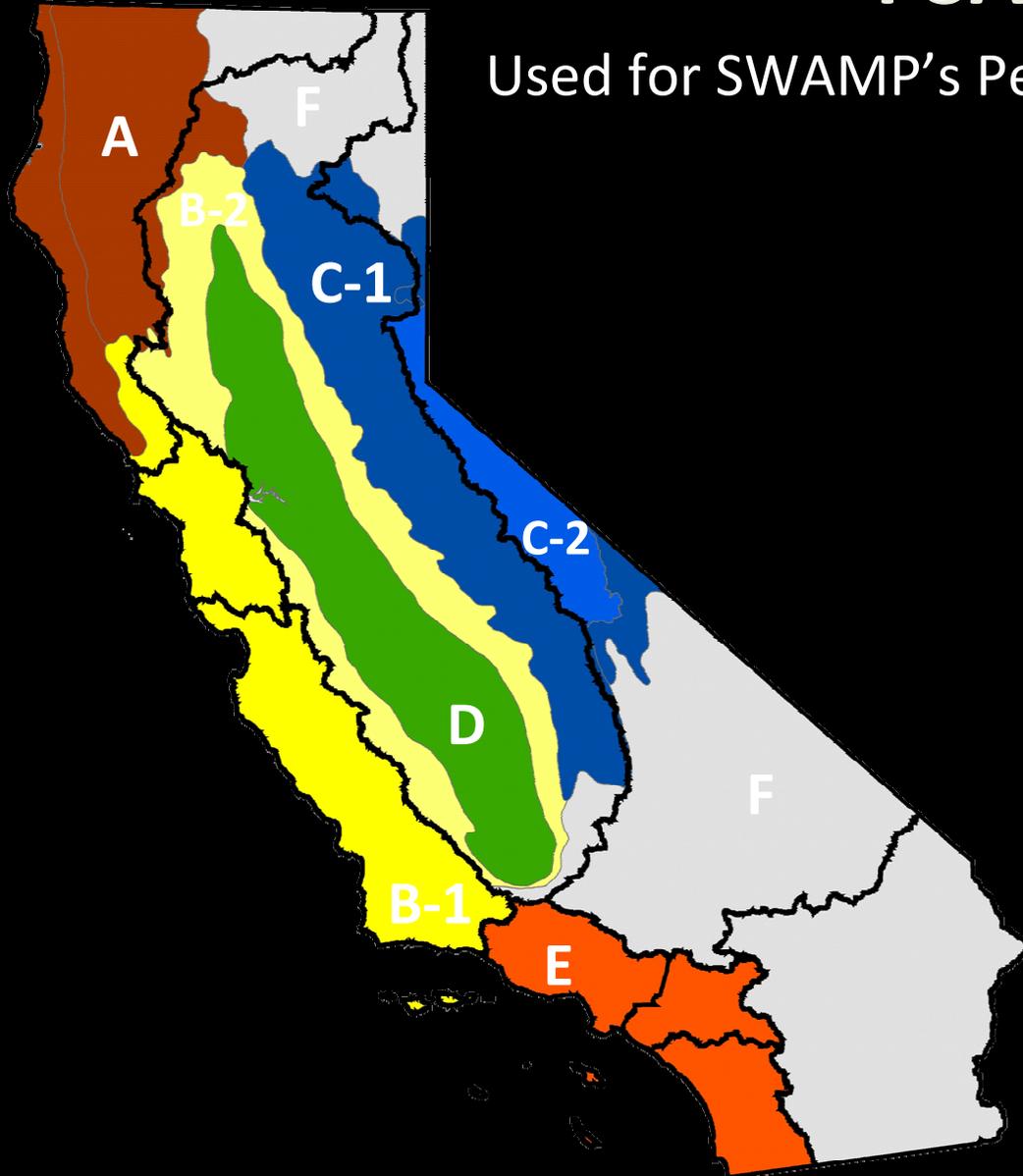
# Questions for Science Panel

- What is your take on the high variability we've seen?
- Can you suggest fruitful variables to explore?
- Should we emphasize certain performance measures and model components (e.g., taxonomic effort levels, predictor characteristics, etc.) to optimize effectiveness in our bio-objectives application?
- How would you like to be involved in the winter?



# PSA Regions

Used for SWAMP's Perennial Streams Assessment



**A = North Coast**

**B = Oak Chaparral**

1 = Coastal Chaparral

2 = Interior Chaparral

**C = Sierra**

1 = Main Sierra

2 = Central Lahontan

**D = Central Valley**

**E = South Coast (SMC)**

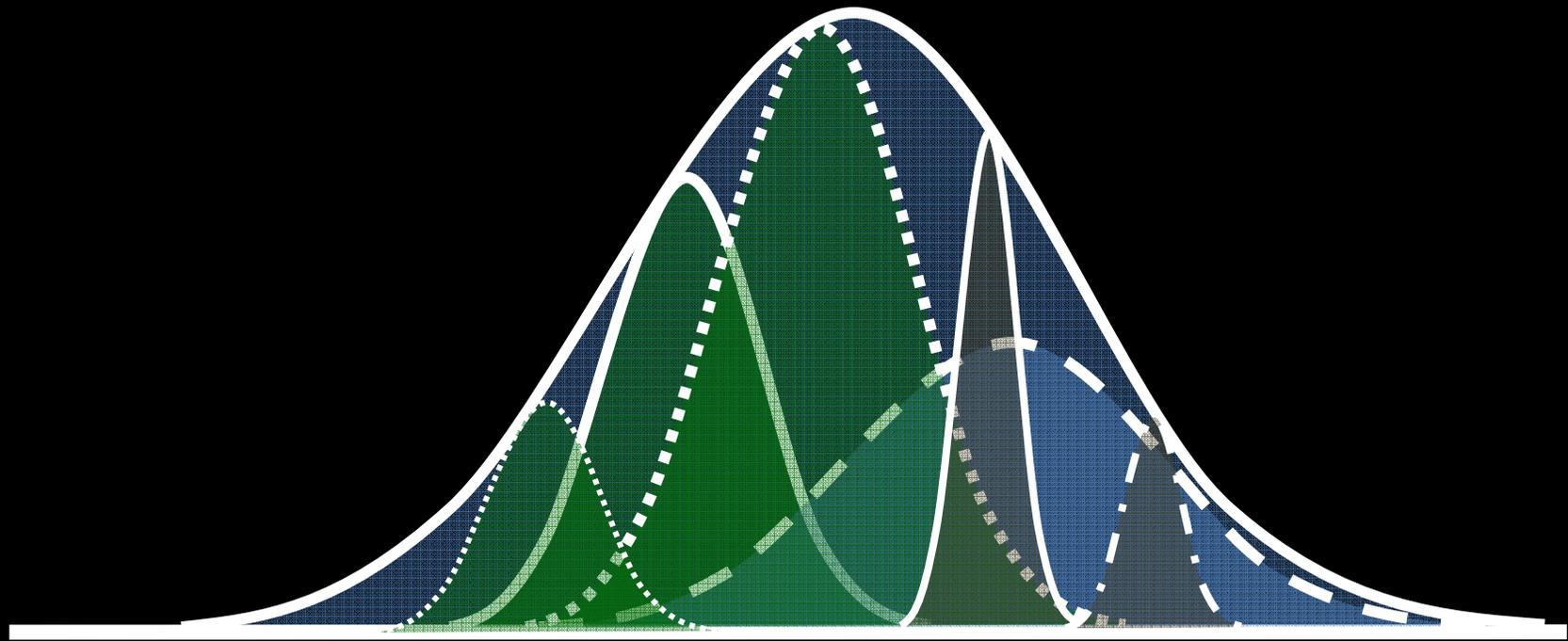
**F = Other:**

- Modoc Plateau
- Deserts

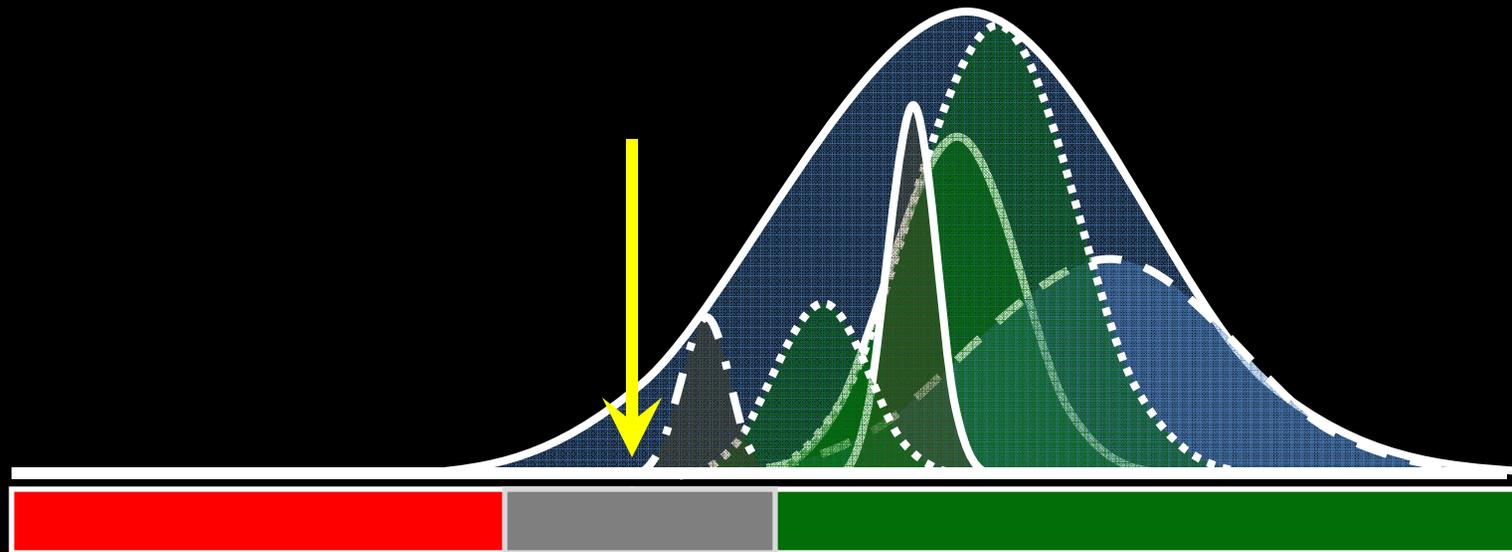
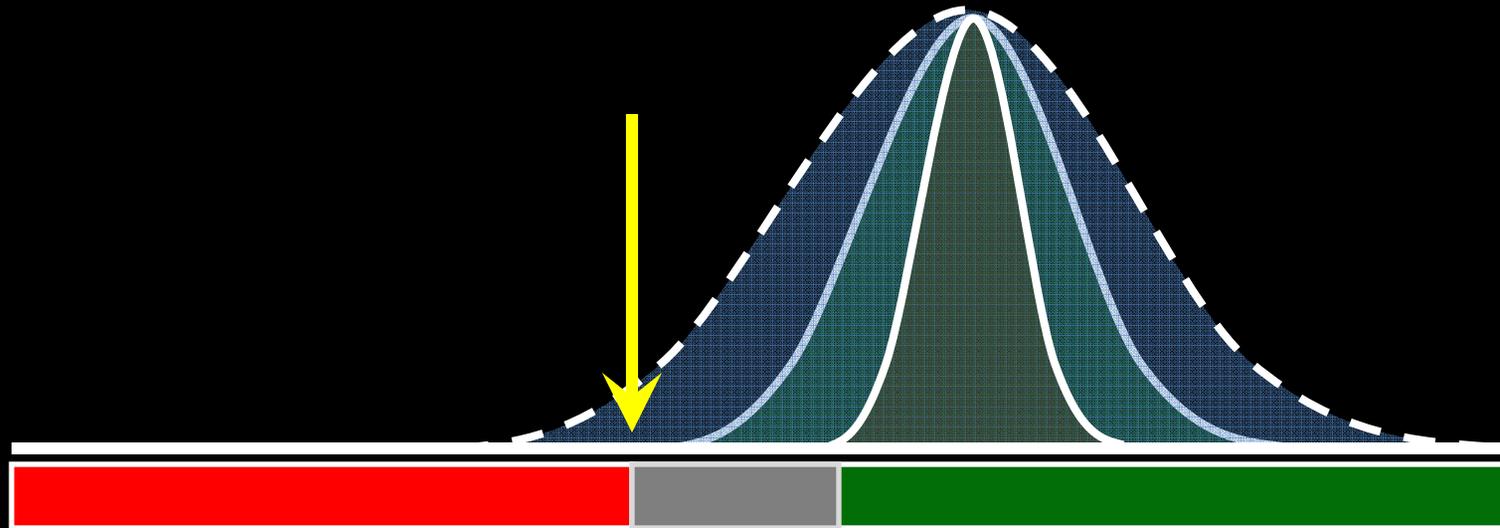
# Final Stressors and Thresholds

Variable	Local Scale	Local Threshold (1k/ 5k)	Watershed Threshold (ws)
% Agricultural <b>or</b> Urban	1k/5k	3 %	10 %
% Agricultural <b>and</b> Urban	1k/5k	5 %	-
% Code 21 (urban grasses)	1k/5k	5 %	10 %
Road Density	1k/5k	2 km/km <sup>2</sup>	2 km/km <sup>2</sup>
Road Crossings	1k/5k	5/10 per km	20 per km
Dam Distance	-	1 km	
% Canals/Pipes	-	10%	
Instream Gravel Mines	5k	0.1/ km	
Producer Mines	5k	1	
Total N	-	3000 µg/L	
Total P	-	500 µg/L	
Conductivity	-	99/1 *	
W1_Hall	-	1.5	

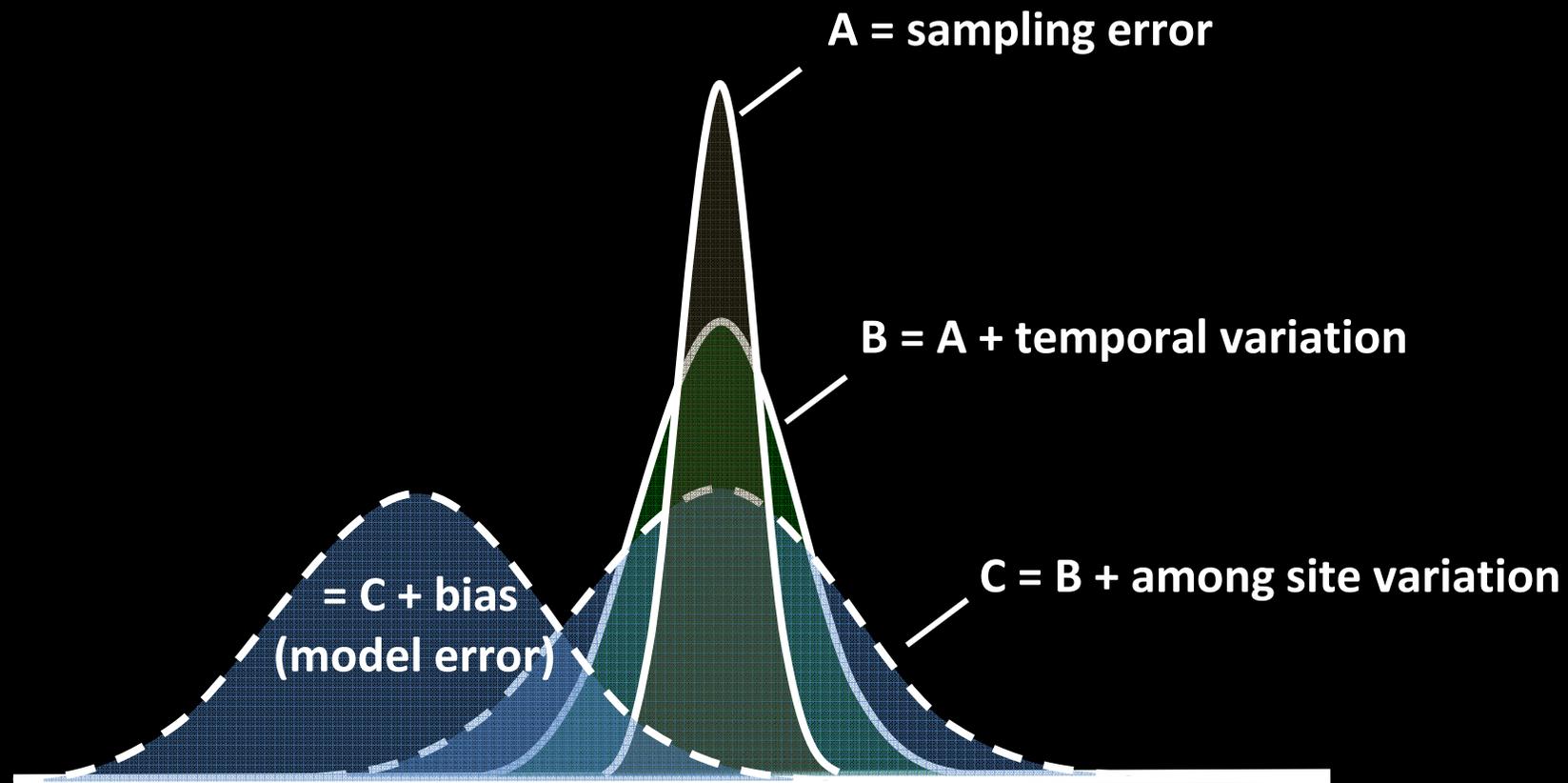
Reference condition is inferred from many reference sites



# Setting the gray area



# Sources of variation in site scores



*(after Hawkins et al. 2010)*